EDITORIAL: PROTEIN MICROARRAYS OVERVIEW

Manuel Fuentes - Centro de Investigación del Cáncer/IBMCC (USAL/CSIC)

Despite revolutionary advances in genomics and our ability to study both genetics and gene expression, the majority of the proteins encoded in our genes has functions that remain unknown. The overwhelming size and complexity of human proteome require very high-throughput techniques for rapid analysis. Around 30% of all the proteins have no function described to them at all, and many of the remaining proteins have functions that are often just "best guesses" based on sequence homology or structure prediction. Despite the significant advancements in molecular biology and genetics tools, this demand has not been satisfied and only a small fraction of the proteome has been understood at the biochemical level. After age of genomics, proteomics seems to be a real key to deal with disease progression in order to generate high-throughput data. Over the last decade, new-generation of high-throughput data has emerged and expanded in the field of proteomics, including next-generation sequencing and mass spectrometry technologies, which have enabled the study of increasing amounts of proteins with less sample requirements. As a consequence, protein microarrays field has been extensively studied during the last years because its capacity to analyze simultaneously hundreds to thousands of proteins in high-throughput format. Biomarkers, particularly those with strong positive and negative predictive value, have many potential uses in the diagnosis and treatment of cancer, including monitoring treatment success, indicating disease progression and detecting early disease. For instance, one potential responds to cancer antigens released by their tumors due to alterations in protein expression, mutation, etc.... The proteomics research in human pathology has focused on the development of clinical applications for accurate diagnosis, early detection and prognosis assessment of human disease due to its potential utility in the identification of candidate biomarkers associated to disease status. Noteworthy, the elucidation of drug´s mechanism by these approaches might lead to further characterization of new therapeutic targets. Hence, one of the most relevant applications of clinical proteomics is the identification and characterization of extremely-low abundant metabolites that might be disease-specific or even prognosis -associated. Therefore, the identification of biomarkers represents the ultimate tool for the improvement of early diagnosis, patient monitoring and/or evaluation of the safety or efficacy of therapeutic strategies. In this way, high-density protein microarrays constitute a novel methodology, biomarker discovery, has made it possible to get better diagnosis, prognosis and stratification of patients with disease proteomics through the study of altered proteins expression of whole-cell, tissues or sub-cellular structures. Moreover, protein microarrays allow the detection of a large number of biomarkers from clinical samples in a very short time. Bearing in mind all these aspects, the field of protein microarrays has been a huge development from technological point of view to clinical applications. In fact, many patents have been issued in both areas. In this special Issue, relevant contributors have participated describing different aspects of protein microarrays, also discussing future directions and pitfalls.